



SEQUENCE LISTING

<110> Hope, Ralph Graham
McLauchlan, John

<120> VIRAL THERAPEUTICS

<130> DY0U17.001CP1

<140> US 09/973,322
<141> 2001-10-09

<150> US 09/201,916
<151> 1998-12-01

<150> GB 9825951.8
<151> 1998-11-26

<160> 22

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 630
<212> DNA
<213> Hepatitis C Virus

<220>
<221> CDS
<222> (43) ... (630)

<400> 1
ggtgcttgcg agtgcccccgg gaggtctcgt agaccgtgca cc atg agc acg aat 54
Met Ser Thr Asn
1

cct aaa cct caa aga aaa acc aaa cgt aac acc aac cgt cgc cca cag 102
Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn Arg Arg Pro Gln
5 10 15 20

gac gtt aag ttc ccg ggt ggc ggt cag atc gtt ggt gga gtt tac ttg 150
Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly Gly Val Tyr Leu
25 30 35

ttg ccg cgc agg ggc cct aga ttg ggt gtg cgc gcg acg agg aag act 198
Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala Thr Arg Lys Thr
40 45 50

tcc gag cgg tcg caa cct cga ggt aga cgt cag cct atc ccc aag gca 246
Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala
55 60 65

cgt cgg ccc aag ggc agg aac tgg gct cag ccc ggg tat cct tgg ccc 294

Arg Arg Pro Lys Gly Arg Asn Trp Ala Gln Pro Gly Tyr Pro Trp Pro				
70	75	80		
ctc tat ggc aat gag ggt tgc ggg tgg gcg gga tgg ctc ctg tcc ccc				342
Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu Ser Pro				
85	90	95	100	
agt ggc tct cgg cct agt tgg ggc ccc aac gac ccc cga cgt agg tcg				390
Ser Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro Arg Arg Arg Ser				
105	110	115		
cgc aat ttg ggt aag gtc atc gat acc ctt acg tgc ggc ttc gtc gat				438
Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Val Asp				
120	125	130		
ctc atg ggg tac ata ccg ctc gtc ggc gcc cct ctt aga ggc gct gcc				486
Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Arg Gly Ala Ala				
135	140	145		
agg gcc ctg gcg cat ggc gtc cggt gtt ctg gaa gac ggt gtg aac tat				534
Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr				
150	155	160		
gca aca ggt aac ctt cct ggt tgc tct ttc tct atc ttc ctt ctg gcc				582
Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala				
165	170	175	180	
ctg ctc tct tgc ctg act gtg ccc gct tca gcc tac caa gtg cgc aac				630
Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Gln Val Arg Asn				
185	190	195		

<210> 2
<211> 60
<212> DNA
<213> Hepatitis C Virus

<220>
<221> CDS
<222> (1)...(60)
<223> Corresponds to aa 125 to 144 of SEQ ID. No. 1

<400> 2
acc ctt acg tgc ggc ttc gtc gat ctc atg ggg tac ata ccg ctc gtc 48
Thr Leu Thr Cys Gly Phe Val Asp Leu Met Gly Tyr Ile Pro Leu Val
1 5 10 15

ggc gcc cct ctt 60
Gly Ala Pro Leu
20

<210> 3
<211> 18

<212> DNA
<213> Hepatitis C Virus

<220>
<221> CDS
<222> (1)...(18)
<223> Corresponds to aa 161-166 of SEQ ID. No. 1

<400> 3
ggt gtg aac tat gca aca
Gly Val Asn Tyr Ala Thr
1 5

18

<210> 4
<211> 1900
<212> DNA
<213> Human

<220>
<221> misc_feature
<222> (1)...(1900)
<223> n = A,T,C or G

<400> 4
cgtcttcggg acgcgccccgc tcttcgcctt tcgctgcagt ccgtcgattt ctttctccag 60
gaagaaaaat ggcatccgtt gcagttgatc cacaaccgag tgtggtgact cgggtggtca 120
acctgcctt ggtgagctcc acgtatgacc tcatgtcctc agcctatctc agtacaaaagg 180
accagtatcc ctacctgaag tctgtgttg agatgscaga gaacgggttg aagaccatca 240
cctccgtggc catgaccagt gctctgccca tcattccagaa gctagagccg caaattgcag 300
ttgccgatac ctatgcctgt aaggggctag acaggattga ggagagactg cctattctga 360
atcagccatc aactcagatt gttgccaatg ccaaaggcgc tggacttggg gcaaaagatg 420
ctgtgacgac tactgtgact gggggccaagg attctgtngc cagcacgatc acaggggtga 480
tggacaagac caaaggggca gtgactggca gtgtggagaa gaccaagtct gtggtcagtg 540
gcagcattaa cacagtcttg gggagtcgga tgatgcagct cgtgagcagt ggcgttagaaa 600
atgcactcac caaatcagag ctgttggtag aacagtacct ccctctcact gaggaagaac 660
tagaaaaaaa agcaaaaaaaaaa gttgaaggat ttgatctggt tcagaagcca agttattatg 720
tttagactggg atccctgtct accaagcttc actccctgtc ctaccagcag gctctcagca 780
gggttaaaga agctaagcaa aaaagccaaac agaccatttc tcagctccat tctactgttc 840
acctgattga atttgcagg aagaatgtgt atagtgc当地 tcagaaaaatt caggatgctc 900
aggataagct ctacctctca tgggttagat gggaaaggag cattggatat gatgatactg 960
atgagtc当地 ctgtgctgag cacatttagt cacgtactct tgcaattgcc cgcaacctga 1020
ctcagcagct ccagaccacg tgccacaccc tcctgtccaa catccaaggt gtaccacaga 1080
acatccaaga tcaagccaaag cacatgggg tgatggcagg cgacatctac tcagtgttcc 1140
gcaatgctgc ctcccttaaa gaagtgtctg acagcctct cacttcttagc aaggggcagc 1200
tgcagaaaaat gaagaatct ttagatgacg tgatggatta tcttgttaac aacacgcccc 1260
tcaactggct ggttaggtccc ttttatcctc agctgactga gtctcagaat gctcaggacc 1320
aagggtgcaga gatggacaag agcagccagg agacccagcg atctgagcat aaaactcatt 1380
aaacctgccc ctatcactag tgcatgctgt ggccagacag atgacacctt ttgttatgtt 1440
gaaattaact tgctaggcaa ccctaaattt ggaagcaagt agcttagtata aaggccctca 1500
attgttagttg tttccagctg aattaagagc tttaaagttt ctggcattag cagatgattt 1560
ctgttcactt ggttagaaaaa gaatgatagg cttgtcagag cctatagcca gaactcagaa 1620
aaaattcaaa tgcacttatg ttctcattct atggccattt tggtgcctct gttactgttt 1680
gtattgaata aaaacatctt catgtgggct ggggtagaaa ctgggtctg ctctgggttg 1740
atctgaaaag gcgtcttcac tgcttatct catgatgctt gcttgtaaaa cttgattta 1800

gttttcatt tctcaaatag gaatactacc tttgaattca ataaaattca ctgcaggata 1860
gaccagttna gnagcaaaca nncangtaca cnnaaganac 1900

<210> 5
<211> 437
<212> PRT
<213> Human

<220>
<221> VARIANT
<222> (1)...(437)
<223> Xaa = Any Amino Acid

<400> 5
Met Ala Ser Val Ala Val Asp Pro Gln Pro Ser Val Val Thr Arg Val
1 5 10 15
Val Asn Leu Pro Leu Val Ser Ser Thr Tyr Asp Leu Met Ser Ser Ala
20 25 30
Tyr Leu Ser Thr Lys Asp Gln Tyr Pro Tyr Leu Lys Ser Val Cys Glu
35 40 45
Met Xaa Glu Asn Gly Val Lys Thr Ile Thr Ser Val Ala Met Thr Ser
50 55 60
Ala Leu Pro Ile Ile Gln Lys Leu Glu Pro Gln Ile Ala Val Ala Asp
65 70 75 80
Thr Tyr Ala Cys Lys Gly Leu Asp Arg Ile Glu Glu Arg Leu Pro Ile
85 90 95
Leu Asn Gln Pro Ser Thr Gln Ile Val Ala Asn Ala Lys Gly Ala Val
100 105 110
Thr Gly Ala Lys Asp Ala Val Thr Thr Val Thr Gly Ala Lys Asp
115 120 125
Ser Val Ala Ser Thr Ile Thr Gly Val Met Asp Lys Thr Lys Gly Ala
130 135 140
Val Thr Gly Ser Val Glu Lys Thr Lys Ser Val Val Ser Gly Ser Ile
145 150 155 160
Asn Thr Val Leu Gly Ser Arg Met Met Gln Leu Val Ser Ser Gly Val
165 170 175
Glu Asn Ala Leu Thr Lys Ser Glu Leu Val Glu Gln Tyr Leu Pro
180 185 190
Leu Thr Glu Glu Leu Glu Lys Glu Ala Lys Lys Val Glu Gly Phe
195 200 205
Asp Leu Val Gln Lys Pro Ser Tyr Tyr Val Arg Leu Gly Ser Leu Ser
210 215 220
Thr Lys Leu His Ser Arg Ala Tyr Gln Gln Ala Leu Ser Arg Val Lys
225 230 235 240
Glu Ala Lys Gln Lys Ser Gln Gln Thr Ile Ser Gln Leu His Ser Thr
245 250 255
Val His Leu Ile Glu Phe Ala Arg Lys Asn Val Tyr Ser Ala Asn Gln
260 265 270
Lys Ile Gln Asp Ala Gln Asp Lys Leu Tyr Leu Ser Trp Val Glu Trp
275 280 285
Lys Arg Ser Ile Gly Tyr Asp Asp Thr Asp Glu Ser His Cys Ala Glu
290 295 300
His Ile Glu Ser Arg Thr Leu Ala Ile Ala Arg Asn Leu Thr Gln Gln
305 310 315 320
Leu Gln Thr Thr Cys His Thr Leu Leu Ser Asn Ile Gln Gly Val Pro

325	330	335
Gln Asn Ile Gln Asp Gln Ala Lys His Met Gly Val Met Ala Gly Asp		
340	345	350
Ile Tyr Ser Val Phe Arg Asn Ala Ala Ser Phe Lys Glu Val Ser Asp		
355	360	365
Ser Leu Leu Thr Ser Ser Lys Gly Gln Leu Gln Lys Met Lys Glu Ser		
370	375	380
Leu Asp Asp Val Met Asp Tyr Leu Val Asn Asn Thr Pro Leu Asn Trp		
385	390	395
Leu Val Gly Pro Phe Tyr Pro Gln Leu Thr Glu Ser Gln Asn Ala Gln		
405	410	415
Asp Gln Gly Ala Glu Met Asp Lys Ser Ser Gln Glu Thr Gln Arg Ser		
420	425	430
Glu His Lys Thr His		
435		

<210> 6

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> branched peptide containing residues 5-27 of HCV
core protein

<221> VARIANT

<222> (1)...(31)

<223> Xaa = Ala or Pro at position 1, and Ile or Asn at
position 12

<400> 6

Xaa Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Xaa Arg Arg Pro Gln			
1	5	10	15

Asp Val Lys Phe Pro Gly Gly Lys Lys Lys Lys Lys Lys Lys Ala			
20	25	30	

<210> 7

<211> 11

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotides used to construct HCV core
protein deletion plasmids

<400> 7

gctgagatct a

11

<210> 8

<211> 29

<212> DNA

<213> Artificial Sequence

<220>
<223> oligonucleotides used to construct HCV core
protein deletion plasmids

<400> 8
gtaaaccttcc tggttgctct tgagatcta 29

<210> 9
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotides used to construct HCV core
protein deletion plasmids

<400> 9
gtaaaccttg agatcta 17

<210> 10
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotides used to construct HCV core
protein deletion plasmids

<400> 10
ctggcgcatt gagatcta 18

<210> 11
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotides used to construct HCV core
protein deletion plasmids

<400> 11
ctggcccatg gtgttaacta tgcaacag 28

<210> 12
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotides used to construct HCV core
protein deletion plasmids

<400> 12
ctggcccatg gcgtccgggt tctggaagac g 31

<210> 13
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotides used to construct HCV core protein deletion plasmids

<400> 13
cgatagaggg cgtgccagg ccctggcgtg agatcta 37

<210> 14
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> HCV1 oligonucleotide for plasmid construction

<400> 14
catggggtag atagcgctcg tcggcgccgc cttaagaggg gctgcgaggg cc 52

<210> 15
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> HCV2 oligonucleotide for plasmid construction

<400> 15
ctagagagcg caagacgccc cgcgtcaccg gcggcg 36

<210> 16
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> primer derived from GBV-B, nucleotides 428-448, for plasmid construction

<400> 16
ggagatctcg tagaccgtag cacatg 26

<210> 17
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> primer derived from GBV-B, nucleotides 842-868, for plasmid construction

<400> 17
ggggatccct agtggacacc gaaccaacca gtagccca 38

<210> 18
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> primer derived from GBV-B, nucleotides 1003-1029,
for plasmid construction

<400> 18
ggggatcctc agatcacaca accaggctcg tgtagg 36

<210> 19
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> primer derived from GBV-B, nucleotides 1618-1639,
for plasmid construction

<400> 19
gggtactcta gagtgatagg cctggtc 27

<210> 20
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> primer derived from GBV-B for plasmid construction

<400> 20
ctagagagcg caagacgccc cgggtcacccg gtggctctcg caatcttgg 49

<210> 21
<211> 156
<212> PRT
<213> GBV-B

<400> 21
Met Pro Val Ile Ser Thr Gln Thr Ser Pro Val Pro Ala Pro Arg Thr
1 5 10 15
Arg Lys Asn Lys Gln Thr Gln Ala Ser Tyr Pro Val Ser Ile Lys Thr
20 25 30
Ser Val Glu Arg Gly Gln Arg Ala Lys Arg Lys Val Gln Arg Asp Ala
35 40 45
Arg Pro Arg Asn Tyr Lys Ile Ala Gly Ile His Asp Gly Leu Gln Thr
50 55 60
Leu Ala Gln Ala Ala Leu Pro Ala His Gly Trp Gly Arg Gln Asp Pro
65 70 75 80
Arg His Lys Ser Arg Asn Leu Gly Ile Leu Leu Asp Tyr Pro Leu Gly

85	90	95
Trp Ile Gly Asp Val Thr Thr His Thr Pro Leu Val Gly Pro Leu Val		
100	105	110
Ala Gly Ala Val Val Arg Pro Val Cys Gln Ile Val Arg Leu Leu Glu		
115	120	125
Asp Gly Val Asn Trp Ala Thr Gly Trp Phe Gly Val His Leu Phe Val		
130	135	140
Val Cys Leu Leu Ser Leu Ala Cys Pro Cys Ser Gly		
145	150	155

<210> 22
<211> 191
<212> PRT
<213> HCV

<400> 22			
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn			
1	5	10	15
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly			
20	25	30	
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala			
35	40	45	
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro			
50	55	60	
Ile Pro Lys Ala Arg Arg Pro Lys Gly Arg Asn Trp Ala Gln Pro Gly			
65	70	75	80
Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp			
85	90	95	
Leu Leu Ser Pro Ser Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro			
100	105	110	
Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys			
115	120	125	
Gly Phe Val Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu			
130	135	140	
Arg Gly Ala Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp			
145	150	155	160
Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile			
165	170	175	
Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala			
180	185	190	